

E. LAZAR

1646

RAW SEQUENCE LISTING  
 PATENT APPLICATION: US/09/405,735

DATE: 05/09/2000  
 TIME: 11:10:38

Input Set : A:\Seqlist.txt  
 Output Set: N:\CRF3\05092000\I405735.raw

4 <110> APPLICANT: Pier, Gerald B.  
 6 <120> TITLE OF INVENTION: Methods and Products for Treating  
 7 Pseudomonas Infection  
 9 <130> FILE REFERENCE: B0801/7155 (HCL)  
 11 <140> CURRENT APPLICATION NUMBER: 09/405,735  
 12 <141> CURRENT FILING DATE: 1999-09-24  
 14 <150> PRIOR APPLICATION NUMBER: US 08/681,838  
 15 <151> PRIOR FILING DATE: 1996-07-29  
 17 <160> NUMBER OF SEQ ID NOS: 4  
 19 <170> SOFTWARE: FastSEQ for Windows Version 3.0

Does Not Comply  
 Corrected Diskette Needed

# ERRORED SEQUENCES

21 <210> SEQ ID NO: 1  
 22 <211> LENGTH: 6129  
 23 <212> TYPE: DNA  
 24 <213> ORGANISM: Homo Sapiens  
 26 <220> FEATURE:  
 27 <221> NAME/KEY: CDS  
 28 <222> LOCATION: (133)...(4575)  
 30 <400> SEQUENCE: 1  
 31 aattggaagc aaatgacatc acagcagggtc agagaaaaag ggttgagcgg caggcaccca 60  
 32 gagtagtagg tctttggcat taggagcttg agcccagacg gccctagcag ggaccccagc 120  
 33 gcccgagaga cc atg cag agg tgc cct ctg gaa aag gcc agc gtt gtc tcc 171  
 34 Met Gln Arg Ser Pro Leu Glu Lys Ala Ser Val Val Ser  
 35 1 5 10  
 37 aaa ctt ttt ttc agc tgg acc aga cca att ttg agg aaa gga tac aga 219  
 38 Lys Leu Phe Phe Ser Trp Thr Arg Pro Ile Leu Arg Lys Gly Tyr Arg  
 39 15 20 25  
 41 cag cgc ctg gaa ttg tca gac ata tac caa atc cct tct gtt gat tct 267  
 42 Gln Arg Leu Glu Leu Ser Asp Ile Tyr Gln Ile Pro Ser Val Asp Ser  
 43 30 35 40 45  
 45 gct gac aat cta tct gaa aaa ttg gaa aga gaa tgg gat aga gag ctg 315  
 46 Ala Asp Asn Leu Ser Glu Lys Leu Glu Arg Glu Trp Asp Arg Glu Leu  
 47 50 55 60  
 49 gct tca aag aaa aat cct aaa ctc att aat gcc ctt cgg cga tgt ttt 363  
 50 Ala Ser Lys Lys Asn Pro Lys Leu Ile Asn Ala Leu Arg Arg Cys Phe  
 51 65 70 75  
 53 ttc tgg aga ttt atg ttc tat gga atc ttt tta tat tta ggg gaa gtc 411  
 54 Phe Trp Arg Phe Met Phe Tyr Gly Ile Phe Leu Tyr Leu Gly Glu Val  
 55 80 85 90  
 57 acc aaa gca gta cag cct ctc tta ctg gga aga atc ata gct tcc tat 459  
 58 Thr Lys Ala Val Gln Pro Leu Leu Leu Gly Arg Ile Ile Ala Ser Tyr  
 59 95 100 105  
 61 gac ccg gat aac aag gag gaa cgc tct atc gcg att tat cta ggc ata 507  
 62 Asp Pro Asp Asn Lys Glu Glu Arg Ser Ile Ala Ile Tyr Leu Gly Ile

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63	110	115	120	125	555
65	ggc tta tgc ctt ctc ttt att gtg agg aca ctg ctc cta cac cca gcc				
66	Gly Leu Cys Leu Leu Phe Ile Val Arg Thr Leu Leu Leu His Pro Ala				
67		130	135	140	603
69	att ttt ggc ctt cat cac att gga atg cag atg aga ata gct atg ttt				
70	Ile Phe Gly Leu His His Ile Gly Met Gln Met Arg Ile Ala Met Phe				
71		145	150	155	651
73	agt ttg att tat aag aag act tta aag ctg tca agc cgt gtt cta gat				
74	Ser Leu Ile Tyr Lys Lys Thr Leu Lys Leu Ser Ser Arg Val Leu Asp				
75		160	165	170	699
77	aaa ata agt att gga caa ctt gtt agt ctc ctt tcc aac aac ctg aac				
78	Lys Ile Ser Ile Gly Gln Leu Val Ser Leu Leu Ser Asn Asn Leu Asn				
79		175	180	185	747
81	aaa ttt gat gaa gga ctt gca ttg gca cat ttc gtg tgg atc gct cct				
82	Lys Phe Asp Glu Gly Leu Ala Leu Ala His Phe Val Trp Ile Ala Pro				
83		190	195	200	795
85	ttg caa gtg gca ctc ctc atg ggg cta atc tgg gag ttg tta cag gcg				
86	Leu Gln Val Ala Leu Leu Met Gly Leu Ile Trp Glu Leu Leu Gln Ala				
87		210	215	220	843
89	tct gcc ttc tgt gga ctt ggt ttc ctg ata gtc ctt gcc ctt ttt cag				
90	Ser Ala Phe Cys Gly Leu Gly Phe Leu Ile Val Leu Ala Leu Phe Gln				
91		225	230	235	891
93	gct ggg cta ggg aga atg atg atg aag tac aga gat cag aga gct ggg				
94	Ala Gly Leu Gly Arg Met Met Met Lys Tyr Arg Asp Gln Arg Ala Gly				
95		240	245	250	939
97	aag atc agt gaa aga ctt gtg att acc tca gaa atg att gaa aat atc				
98	Lys Ile Ser Glu Arg Leu Val Ile Thr Ser Glu Met Ile Glu Asn Ile				
99		255	260	265	987
101	caa tct gtt aag gca tac tgc tgg gaa gaa gca atg gaa aaa atg att				
102	Gln Ser Val Lys Ala Tyr Cys Trp Glu Glu Ala Met Glu Lys Met Ile				
103		270	275	280	1035
105	gaa aac tta aga caa aca gaa ctg aaa ctg act cgg aag gca gcc tat				
106	Glu Asn Leu Arg Gln Thr Glu Leu Lys Leu Thr Arg Lys Ala Ala Tyr				
107		290	295	300	1083
109	gtg aga tac ttc aat agc tca gcc ttc ttc ttc tca ggg ttc ttt gtg				
110	Val Arg Tyr Phe Asn Ser Ser Ala Phe Phe Phe Ser Gly Phe Phe Val				
111		305	310	315	1131
113	gtg ttt tta tct gtg ctt ccc tat gca cta atc aaa gga atc atc ctc				
114	Val Phe Leu Ser Val Leu Pro Tyr Ala Leu Ile Lys Gly Ile Ile Leu				
115		320	325	330	1179
117	cgg aaa ata ttc acc acc atc tca ttc tgc att gtt ctg cgc atg gcg				
118	Arg Lys Ile Phe Thr Thr Ile Ser Phe Cys Ile Val Leu Arg Met Ala				
119		335	340	345	1227
121	gtc act cgg caa ttt ccc tgg gct gta caa aca tgg tat gac tct ctt				
122	Val Thr Arg Gln Phe Pro Trp Ala Val Gln Thr Trp Tyr Asp Ser Leu				
123		350	355	360	1275
125	gga gca ata aac aaa ata cag gat ttc tta caa aag caa gaa tat aag				
126	Gly Ala Ile Asn Lys Ile Gln Asp Phe Leu Gln Lys Gln Glu Tyr Lys				
127		370	375	380	

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129	aca ttg gaa tat aac tta acg act aca gaa gta gtg atg gag aat gta	1323
130	Thr Leu Glu Tyr Asn Leu Thr Thr Thr Glu Val Val Met Glu Asn Val	
131	385 390 395	
133	aca gcc ttc tgg gag gag gga ttt ggg gaa tta ttt gag aaa gca aaa	1371
134	Thr Ala Phe Trp Glu Glu Gly Phe Gly Glu Leu Phe Glu Lys Ala Lys	
135	400 405 410	
137	caa aac aat aac aat aga aaa act tct aat ggt gat gac agc ctc ttc	1419
138	Gln Asn Asn Asn Asn Arg Lys Thr Ser Asn Gly Asp Asp Ser Leu Phe	
139	415 420 425	
141	ttc agt aat ttc tca ctt ctt ggt act cct gtc ctg aaa gat att aat	1467
142	Phe Ser Asn Phe Ser Leu Leu Gly Thr Pro Val Leu Lys Asp Ile Asn	
143	430 435 440 445	
145	ttc aag ata gaa aga gga cag ttg ttg gcg gtt gct gga tcc act gga	1515
146	Phe Lys Ile Glu Arg Gly Gln Leu Leu Ala Val Ala Gly Ser Thr Gly	
147	450 455 460	
149	gca ggc aag act tca ctt cta atg atg att atg gga gaa ctg gag cct	1563
150	Ala Gly Lys Thr Ser Leu Leu Met Met Ile Met Gly Glu Leu Glu Pro	
151	465 470 475	
153	tca gag ggt aaa att aag cac agt gga aga att tca ttc tgt tct cag	1611
154	Ser Glu Gly Lys Ile Lys His Ser Gly Arg Ile Ser Phe Cys Ser Gln	
155	480 485 490	
157	ttt tcc tgg att atg cct gcc acc att aaa gaa aat atc atc ttt ggt	1659
158	Phe Ser Trp Ile Met Pro Gly Thr Ile Lys Glu Asn Ile Ile Phe Gly	
159	495 500 505	
161	gtt tcc tat gat gaa tat aga tac aga agc gtc atc aaa gca tgc caa	1707
162	Val Ser Tyr Asp Glu Tyr Arg Tyr Arg Ser Val Ile Lys Ala Cys Gln	
163	510 515 520 525	
165	cta gaa gag gac atc tcc aag ttt gca gag aaa gac aat ata gtt ctt	1755
166	Leu Glu Glu Asp Ile Ser Lys Phe Ala Glu Lys Asp Asn Ile Val Leu	
167	530 535 540	
169	gga gaa ggt gga atc aca ctg agt gga ggt caa cga gca aga att tct	1803
170	Gly Glu Gly Gly Ile Thr Leu Ser Gly Gly Gln Arg Ala Arg Ile Ser	
171	545 550 555	
173	tta gca aga gca gta tac aaa gat gct gat ttg tat tta tta gac tct	1851
174	Leu Ala Arg Ala Val Tyr Lys Asp Ala Asp Leu Tyr Leu Leu Asp Ser	
175	560 565 570	
177	cct ttt gga tac cta gat gtt tta aca gaa aaa gaa ata ttt gaa agc	1899
178	Pro Phe Gly Tyr Leu Asp Val Leu Thr Glu Lys Glu Ile Phe Glu Ser	
179	575 580 585	
181	tgt gtc tgt aaa ctg atg gct aac aaa act agg att ttg gtc act tct	1947
182	Cys Val Cys Lys Leu Met Ala Asn Lys Thr Arg Ile Leu Val Thr Ser	
183	590 595 600 605	
185	aaa atg gaa cat tta aag aaa gct gac aaa ata tta att ttg aat gaa	1995
186	Lys Met Glu His Leu Lys Lys Ala Asp Lys Ile Leu Ile Leu Asn Glu	
187	610 615 620	
189	ggt agc agc tat ttt tat ggg aca ttt tca gaa ctc caa aat cta cag	2043
190	Gly Ser Ser Tyr Phe Tyr Gly Thr Ser Glu Leu Gln Asn Leu Gln	
191	625 630 635	
193	cca gac ttt agc tca aaa ctc atg gga tgt gat tct ttc gac caa ttt	2091

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194 Pro Asp Phe Ser Ser Lys Leu Met Gly Cys Asp Ser Phe Asp Gln Phe
195          640          645          650
197 agt gca gaa aga aga aat tca atc cta act gag acc tta cac cgt ttc 2139
198 Ser Ala Glu Arg Arg Asn Ser Ile Leu Thr Glu Thr Leu His Arg Phe
199          655          660          665
201 tca tta gaa gga gat gct cct gtc tcc tgg aca gaa aca aaa aaa caa 2187
202 Ser Leu Glu Gly Asp Ala Pro Val Ser Trp Thr Glu Thr Lys Lys Gln
203          670          675          680          685
205 tct ttt aaa cag act gga gag ttt ggg gaa aaa agg aag aat tct att 2235
206 Ser Phe Lys Gln Thr Gly Glu Phe Gly Glu Lys Arg Lys Asn Ser Ile
207          690          695          700
209 ctc aat cca atc aac tct ata cga aaa ttt tcc att gtg caa aag act 2283
210 Leu Asn Pro Ile Asn Ser Ile Arg Lys Phe Ser Ile Val Gln Lys Thr
211          705          710          715
213 ccc tta caa atg aat ggc atc gaa gag gat tct gat gag cct tta gag 2331
214 Pro Leu Gln Met Asn Gly Ile Glu Glu Asp Ser Asp Glu Pro Leu Glu
215          720          725          730
217 aga agg ctg tcc tta gta cca gat tct gag cag gga gag gcg ata ctg 2379
218 Arg Arg Leu Ser Leu Val Pro Asp Ser Glu Gln Gly Glu Ala Ile Leu
219          735          740          745
221 cct cgc atc agc gtg atc agc act ggc ccc acg ctt cag gca cga agg 2427
222 Pro Arg Ile Ser Val Ile Ser Thr Gly Pro Thr Leu Gln Ala Arg Arg
223          750          755          760          765
225 agg cag tct gtc ctg aac ctg atg aca cac tca gtt aac caa ggt cag 2475
226 Arg Gln Ser Val Leu Asn Leu Met Thr His Ser Val Asn Gln Gly Gln
227          770          775          780
229 aac att cac cga aag aca aca gca tcc aca cga aaa gtg tca ctg gcc 2523
230 Asn Ile His Arg Lys Thr Thr Ala Ser Thr Arg Lys Val Ser Leu Ala
231          785          790          795
233 cct cag gca aac ttg act gaa ctg gat ata tat tca aga agg tta tct 2571
234 Pro Gln Ala Asn Leu Thr Glu Leu Asp Ile Tyr Ser Arg Arg Leu Ser
235          800          805          810
237 caa gaa act ggc ttg gaa ata agt gaa gaa att aac gaa gaa gac tta 2619
238 Gln Glu Thr Gly Leu Glu Ile Ser Glu Glu Ile Asn Glu Glu Asp Leu
239          815          820          825
241 aag gag tgc ctt ttt gat gat atg gag agc ata cca gca gtg act aca 2667
242 Lys Glu Cys Leu Phe Asp Met Glu Ser Ile Pro Ala Val Thr Thr
243          830          835          840          845
245 tgg aac aca tac ctt cga tat att act gtc cac aag agc tta att ttt 2715
246 Trp Asn Thr Tyr Leu Arg Tyr Ile Thr Val His Lys Ser Leu Ile Phe
247          850          855          860
249 gtg cta att tgg tgc tta gta att ttt ctg gca gag gtg gct gct tct 2763
250 Val Leu Ile Trp Cys Leu Val Ile Phe Leu Ala Glu Val Ala Ala Ser
251          865          870          875
253 ttg gtt gtg ctg tgg ctc ctt gga aac act cct ctt caa gac aaa ggg 2811
254 Leu Val Val Leu Trp Leu Leu Gly Asn Thr Pro Leu Gln Asp Lys Gly
255          880          885          890
257 aat agt act cat agt aga aat aac agc tat gca gtg att atc acc agc 2859
258 Asn Ser Thr His Ser Arg Asn Asn Ser Tyr Ala Val Ile Ile Thr Ser

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259      895      900      905
261 acc agt tcg tat tat gtg ttt tac att tac gtg gga gta gcc gac act 2907
262 Thr Ser Ser Tyr Tyr Val Phe Tyr Ile Tyr Val Gly Val Ala Asp Thr
263 910      915      920      925
265 ttg ctt gct atg gga ttc ttc aga ggt cta cca ctg gtg cat act cta 2955
266 Leu Leu Ala Met Gly Phe Phe Arg Gly Leu Pro Leu Val His Thr Leu
267      930      935      940
269 atc aca gtg tcg aaa att tta cac cac aaa atg tta cat tct gtt ctt 3003
270 Ile Thr Val Ser Lys Ile Leu His His Lys Met Leu His Ser Val Leu
271      945      950      955
273 caa gca cct atg tca acc ctc aac acg ttg aaa gca ggt ggg att ctt 3051
274 Gln Ala Pro Met Ser Thr Leu Asn Thr Leu Lys Ala Gly Gly Ile Leu
275      960      965      970
277 aat aga ttc tcc aaa gat ata gca att ttg gat gac ctt ctg cct ctt 3099
278 Asn Arg Phe Ser Lys Asp Ile Ala Ile Leu Asp Asp Leu Leu Pro Leu
279      975      980      985
281 acc ata ttt gac ttc atc cag ttg tta tta att gtg att gga gct ata 3147
282 Thr Ile Phe Asp Phe Ile Gln Leu Leu Ile Val Ile Gly Ala Ile
283 990      995      1000      1005
285 gca gtt gtc gca gtt tta caa ccc tac atc ttt gtt gca aca gtg cca 3195
286 Ala Val Val Ala Val Leu Gln Pro Tyr Ile Phe Val Ala Thr Val Pro
287      1010      1015      1020
289 gtg ata gtg gct ttt att atg ttg aga gca tat ttc ctc caa acc tca 3243
290 Val Ile Val Ala Phe Ile Met Leu Arg Ala Tyr Phe Leu Gln Thr Ser
291      1025      1030      1035
293 cag caa ctc aaa caa ctg gaa tct gaa ggc agg agt cca att ttc act 3291
294 Gln Gln Leu Lys Gln Leu Glu Ser Glu Gly Arg Ser Pro Ile Phe Thr
295      1040      1045      1050
297 cat ctt gtt aca agc tta aaa gga cta tgg aca ctt cgt gcc ttc gga 3339
298 His Leu Val Thr Ser Leu Lys Gly Leu Trp Thr Leu Arg Ala Phe Gly
299      1055      1060      1065
301 cgg cag cct tac ttt gaa act ctg ttc cac aaa gct ctg aat tta cat 3387
302 Arg Gln Pro Tyr Phe Glu Thr Leu Phe His Lys Ala Leu Asn Leu His
W--> 303 1070      1075      1080      1085
305 act gcc aac tgg ttc ttg tac ctg tca aca ctg cgc tgg ttc caa atg 3435
306 Thr Ala Asn Trp Phe Leu Tyr Leu Ser Thr Leu Arg Trp Phe Gln Met
307      1090      1095      1100
309 aga ata gaa atg att ttt gtc atc ttc ttc att gct gtt acc ttc att 3483
310 Arg Ile Glu Met Ile Phe Val Ile Phe Phe Ile Ala Val Thr Phe Ile
311      1105      1110      1115
313 tcc att tta aca aca gga gaa gga gaa gga aga gtt ggt att atc ctg 3531
314 Ser Ile Leu Thr Thr Gly Glu Gly Glu Gly Arg Val Gly Ile Ile Leu
315      1120      1125      1130
317 act tta gcc atg aat atc atg agt aca ttg cag tgg gct gta aac tcc 3579
318 Thr Leu Ala Met Asn Ile Met Ser Thr Leu Gln Trp Ala Val Asn Ser
319      1135      1140      1145
321 agc ata gat gtg gat agc ttg atg cga tct gtg agc cga gtc ttt aag 3627
322 Ser Ile Asp Val Asp Ser Leu Met Arg Ser Val Ser Arg Val Phe Lys
W--> 323 1150      1155      1160      1165

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325 ttc att gac atg cca aca gaa ggt aaa cct acc aag tca acc aaa cca 3675
326 Phe Ile Asp Met Pro Thr Glu Gly Lys Pro Thr Lys Ser Thr Lys Pro
327 1170 1175 1180
329 tac aag aat ggc caa ctc tgc aaa gtt atg att att gag aat tca cac 3723
330 Tyr Lys Asn Gly Gln Leu Ser Lys Val Met Ile Ile Glu Asn Ser His
331 1185 1190 1195
333 gtg aag aaa gat gac atc tgg ccc tca ggg ggc caa atg act gtc aaa 3771
334 Val Lys Lys Asp Asp Ile Trp Pro Ser Gly Gly Gln Met Thr Val Lys
335 1200 1205 1210
337 gat ctc aca gca aaa tac aca gaa ggt gga aat gcc ata tta gag aac 3819
338 Asp Leu Thr Ala Lys Tyr Thr Glu Gly Gly Asn Ala Ile Leu Glu Asn
339 1215 1220 1225
341 att tcc ttc tca ata agt cct ggc cag agg gtg ggc ctc ttg gga aga 3867
342 Ile Ser Phe Ser Ile Ser Pro Gly Gln Arg Val Gly Leu Leu Gly Arg
343 W--> 230 1235 1240 1245
345 act gga tca ggg aag agt act ttg tta tca gct ttt ttg aga cta ctg 3915
346 Thr Gly Ser Gly Lys Ser Thr Leu Leu Ser Ala Phe Leu Arg Leu Leu
347 1250 1255 1260
349 aac act gaa gga gaa atc cag atc gat ggt gtg tct tgg gat tca ata 3963
350 Asn Thr Glu Gly Glu Ile Gln Ile Asp Gly Val Ser Trp Asp Ser Ile
351 1265 1270 1275
353 act ttg caa cag tgg agg aaa gcc ttt gga gtg ata cca cag aaa gta 4011
354 Thr Leu Gln Gln Trp Arg Lys Ala Phe Gly Val Ile Pro Gln Lys Val
355 1280 1285 1290
357 ttt att ttt tct gga aca ttt aga aaa aac ttg gat ccc tat gaa cag 4059
358 Phe Ile Phe Ser Gly Thr Phe Arg Lys Asn Leu Asp Pro Tyr Glu Gln
359 1295 1300 1305
361 tgg agt gat caa gaa ata tgg aaa gtt gca gat gag gtt ggg ctc aga 4107
362 Trp Ser Asp Gln Glu Ile Trp Lys Val Ala Asp Glu Val Gly Leu Arg
363 W--> 310 1315 1320 1325
365 tct gtg ata gaa cag ttt cct ggg aag ctt gac ttt gtc ctt gtg gat 4155
366 Ser Val Ile Glu Gln Phe Pro Gly Lys Leu Asp Phe Val Leu Val Asp
367 1330 1335 1340
369 ggg ggc tgt gtc cta agc cat ggc cac aag cag ttg atg tgc ttg gct 4203
370 Gly Gly Cys Val Leu Ser His Gly His Lys Gln Leu Met Cys Leu Ala
371 1345 1350 1355
373 aga tct gtt ctc agt aag gcg aag atc ttg ctg ctt gat gaa ccc agt 4251
374 Arg Ser Val Leu Ser Lys Ala Lys Ile Leu Leu Leu Asp Glu Pro Ser
375 1360 1365 1370
377 gct cat ttg gat cca gta aca tac caa ata att aga aga act cta aaa 4299
378 Ala His Leu Asp Pro Val Thr Tyr Gln Ile Ile Arg Arg Thr Leu Lys
379 1375 1380 1385
381 caa gca ttt gct gat tgc aca gta att ctc tgt gaa cac agg ata gaa 4347
382 Gln Ala Phe Ala Asp Cys Thr Val Ile Leu Cys Glu His Arg Ile Glu
383 W--> 390 1395 1400 1405
385 gca atg ctg gaa tgc caa caa ttt ttg gtc ata gaa gag aac aaa gtg 4395
386 Ala Met Leu Glu Cys Gln Gln Phe Leu Val Ile Glu Glu Asn Lys Val
387 1410 1415 1420
389 cgg cag tac gat tcc atc cag aaa ctg ctg aac gag agg agc ctc ttc 4443

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390 Arg Gln Tyr Asp Ser Ile Gln Lys Leu Leu Asn Glu Arg Ser Leu Phe
391      1425      1430      1435      4491
393 cgg caa gcc atc agc ccc tcc gac agg gtg aag ctc ttt ccc cac cgg
394 Arg Gln Ala Ile Ser Pro Ser Asp Arg Val Lys Leu Phe Pro His Arg
395      1440      1445      1450      4539
397 aac tca agc aag tgc aag tct aag ccc cag att gct gct ctg aaa gag
398 Asn Ser Ser Lys Cys Lys Ser Lys Pro Gln Ile Ala Ala Leu Lys Glu
399      1455      1460      1465      4585
401 gag aca gaa gaa gag gtg caa gat aca agg ctt tag agagcagcat
402 Glu Thr Glu Glu Glu Val Gln Asp Thr Arg Leu *
W--> 403 470      1475      1480      4645
405 aaatgttgac atgggacatt tgctcatgga attggagctc gtgggacagt caccctcatgg 4705
406 aattggagct cgtggaacag ttacctctgc ctcagaaaaac aaggatgaat taagtttttt 4765
407 tttaaaaaag aaacatttgg taagggaagt tgaggacact gatatgggtc ttgataaatg 4825
408 gcttcctggc aatagtcaaa ttgtgtgaaa ggtacttcaa atccttgaag atttaccact 4885
409 tgtgttttgc aagccagatt ttcttgaaaa cccttgccat gtgctagtaa ttggaaaggc 4945
410 agctctaaat gtcaatcagc ctagttagtc agcttattgt ctagtgaaac tcgttaattt 5005
411 gtagtggttg agaagaactg aaatcatact tcttaggggt atgattaaat aatgataact 5065
412 ggaacttca gcggtttata taagcttgta ttcttttttc tctctctcc ccatgatgtt 5125
413 tagaaacaca actatattgt ttgtaagca ttccaactat ctcatttcca agcaagtatt 5185
414 agaataccac aggaaccaca agactgcaca tcaaaatatg cccatttcaa catctagtga 5245
415 gcagtcagga aagagaactt ccagatcctg gaaatcaggg ttagtattgt ccaggtctac 5305
416 caaaaatctc aatattttag ataatacaca tacatccctt acctgggaaa gggctgttat 5365
417 aatctttcac aggggacagg atggttccct tgatgaagaa gttgatatgc aagtatgtta 5425
418 ctccagaag tgacaagctc acagacctt gaactagagt ttagctggaa aagtatgtta 5485
419 gtgcaaattg tcacaggaca gcccttcttt ccacagaagc tccaggtaga ggggtgtgaa 5545
420 gtagataggc catgggcact gtgggtagac acacatgaag tccaagcatt tagatgtata 5605
421 ggttgatggt ggtatgtttt caggctagat gtatgtactt catgctgtct acactaagag 5665
422 agaatgagag acacactgaa gaagcaccaa tcatgaatta gttttatatg cttctgtttt 5725
423 ataattttgt gaagcaaat ttttctcta ggaaatattt attttaataa tgtttcaaac 5785
424 atataattaca atgctgtatt ttaaaagaat gattatgaat tacatttgta taaaataatt 5845
425 tttatatttg aaatattgac ttttatggc actagtattt ttatgaaata ttatgttaaa 5905
426 actgggacag gggagaacct aggggtatat taaccaggg ccatgaatca ccttttggtc 5965
427 tggagggaag ccttggggct gatcgagttg ttgccacag ctgtatgatt cccagccaga 6025
428 cacagcctct tagatgcagt tctgaagaag atggtaccac cagctctgact gtttccatca 6085
429 aggttacact gccttctcaa ctccaaactg actcttaaga agactgcatt atatttatta
E--> 430 ctgtaagaaa atatcacttg tcaataaaat ccatacattt gtgt
432 <210> SEQ ID NO: 2
433 <211> LENGTH: 1480
434 <212> TYPE: PRT
435 <213> ORGANISM: Homo Sapiens
437 <400> SEQUENCE: 2
438 Met Gln Arg Ser Pro Leu Glu Lys Ala Ser Val Val Ser Lys Leu Phe
439      1      5      10      15
440 Phe Ser Trp Thr Arg Pro Ile Leu Arg Lys Gly Tyr Arg Gln Arg Leu
441      20      25      30
442 Glu Leu Ser Asp Ile Tyr Gln Ile Pro Ser Val Asp Ser Ala Asp Asn
443      35      40      45
444 Leu Ser Glu Lys Leu Glu Arg Glu Trp Asp Arg Glu Leu Ala Ser Lys

```

6129

RAW SEQUENCE LISTING  
 PATENT APPLICATION: US/09/405,735

DATE: 05/09/2000  
 TIME: 11:10:38

Input Set : A:\Seqlist.txt  
 Output Set : N:\CRF3\05092000\I405735.raw

```

445          50          55          60
446 Lys Asn Pro Lys Leu Ile Asn Ala Leu Arg Arg Cys Phe Phe Trp Arg
447 65          70          75          80
448 Phe Met Phe Tyr Gly Ile Phe Leu Tyr Leu Gly Glu Val Thr Lys Ala
449          85          90          95
450 Val Gln Pro Leu Leu Leu Gly Arg Ile Ile Ala Ser Tyr Asp Pro Asp
451          100          105          110
452 Asn Lys Glu Glu Arg Ser Ile Ala Ile Tyr Leu Gly Ile Gly Leu Cys
453          115          120          125
454 Leu Leu Phe Ile Val Arg Thr Leu Leu His Pro Ala Ile Phe Gly
455          130          135          140
456 Leu His His Ile Gly Met Gln Met Arg Ile Ala Met Phe Ser Leu Ile
457 145          150          155          160
458 Tyr Lys Lys Thr Leu Lys Leu Ser Ser Arg Val Leu Asp Lys Ile Ser
459          165          170          175
460 Ile Gly Gln Leu Val Ser Leu Leu Ser Asn Asn Leu Asn Lys Phe Asp
461          180          185          190
462 Glu Gly Leu Ala Leu Ala His Phe Val Trp Ile Ala Pro Leu Gln Val
463          195          200          205
464 Ala Leu Leu Met Gly Leu Ile Trp Glu Leu Leu Gln Ala Ser Ala Phe
465          210          215          220
466 Cys Gly Leu Gly Phe Leu Ile Val Leu Ala Leu Phe Gln Ala Gly Leu
467 225          230          235          240
468 Gly Arg Met Met Met Lys Tyr Arg Asp Gln Arg Ala Gly Lys Ile Ser
469          245          250          255
470 Glu Arg Leu Val Ile Thr Ser Glu Met Ile Glu Asn Ile Gln Ser Val
471          260          265          270
472 Lys Ala Tyr Cys Trp Glu Glu Ala Met Glu Lys Met Ile Glu Asn Leu
473          275          280          285
474 Arg Gln Thr Glu Leu Lys Leu Thr Arg Lys Ala Ala Tyr Val Arg Tyr
475          290          295          300
476 Phe Asn Ser Ser Ala Phe Phe Phe Ser Gly Phe Phe Val Val Phe Leu
477 305          310          315          320
478 Ser Val Leu Pro Tyr Ala Leu Ile Lys Gly Ile Ile Leu Arg Lys Ile
479          325          330          335
480 Phe Thr Thr Ile Ser Phe Cys Ile Val Leu Arg Met Ala Val Thr Arg
481          340          345          350
482 Gln Phe Pro Trp Ala Val Gln Thr Trp Tyr Asp Ser Leu Gly Ala Ile
483          355          360          365
484 Asn Lys Ile Gln Asp Phe Leu Gln Lys Gln Glu Tyr Lys Thr Leu Glu
485          370          375          380
486 Tyr Asn Leu Thr Thr Thr Glu Val Val Met Glu Asn Val Thr Ala Phe
487 385          390          395          400
488 Trp Glu Glu Gly Phe Gly Glu Leu Phe Glu Lys Ala Lys Gln Asn Asn
489          405          410          415
490 Asn Asn Arg Lys Thr Ser Asn Gly Asp Asp Ser Leu Phe Phe Ser Asn
491          420          425          430
492 Phe Ser Leu Leu Gly Thr Pro Val Leu Lys Asp Ile Asn Phe Lys Ile
493          435          440          445

```



RAW SEQUENCE LISTING  
 PATENT APPLICATION: US/09/405,735

DATE: 05/09/2000  
 TIME: 11:10:38

Input Set : A:\Seqlist.txt  
 Output Set: N:\CRF3\05092000\I405735.raw

```

494 Glu Arg Gly Gln Leu Leu Ala Val Ala Gly Ser Thr Gly Ala Gly Lys
495      450      455      460
496 Thr Ser Leu Leu Met Met Ile Met Gly Glu Leu Glu Pro Ser Glu Gly
497 465      470      475      480
498 Lys Ile Lys His Ser Gly Arg Ile Ser Phe Cys Ser Gln Phe Ser Trp
499      485      490      495
500 Ile Met Pro Gly Thr Ile Lys Glu Asn Ile Ile Phe Gly Val Ser Tyr
501      500      505      510
502 Asp Glu Tyr Arg Tyr Arg Ser Val Ile Lys Ala Cys Gln Leu Glu Glu
503      515      520      525
504 Asp Ile Ser Lys Phe Ala Glu Lys Asp Asn Ile Val Leu Gly Glu Gly
505      530      535      540
506 Gly Ile Thr Leu Ser Gly Gly Gln Arg Ala Arg Ile Ser Leu Ala Arg
507 545      550      555      560
508 Ala Val Tyr Lys Asp Ala Asp Leu Tyr Leu Leu Asp Ser Pro Phe Gly
509      565      570      575
510 Tyr Leu Asp Val Leu Thr Glu Lys Glu Ile Phe Glu Ser Cys Val Cys
511      580      585      590
512 Lys Leu Met Ala Asn Lys Thr Arg Ile Leu Val Thr Ser Lys Met Glu
513      595      600      605
514 His Leu Lys Lys Ala Asp Lys Ile Leu Ile Leu Asn Glu Gly Ser Ser
515      610      615      620
516 Tyr Phe Tyr Gly Thr Phe Ser Glu Leu Gln Asn Leu Gln Pro Asp Phe
517 625      630      635      640
518 Ser Ser Lys Leu Met Gly Cys Asp Ser Phe Asp Gln Phe Ser Ala Glu
519      645      650      655
520 Arg Arg Asn Ser Ile Leu Thr Glu Thr Leu His Arg Phe Ser Leu Glu
521      660      665      670
522 Gly Asp Ala Pro Val Ser Trp Thr Glu Thr Lys Lys Gln Ser Phe Lys
523      675      680      685
524 Gln Thr Gly Glu Phe Gly Glu Lys Arg Lys Asn Ser Ile Leu Asn Pro
525      690      695      700
526 Ile Asn Ser Ile Arg Lys Phe Ser Ile Val Gln Lys Thr Pro Leu Gln
527 705      710      715      720
528 Met Asn Gly Ile Glu Glu Asp Ser Asp Glu Pro Leu Glu Arg Arg Leu
529      725      730      735
530 Ser Leu Val Pro Asp Ser Glu Gln Gly Glu Ala Ile Leu Pro Arg Ile
531      740      745      750
532 Ser Val Ile Ser Thr Gly Pro Thr Leu Gln Ala Arg Arg Arg Gln Ser
533      755      760      765
534 Val Leu Asn Leu Met Thr His Ser Val Asn Gln Gly Gln Asn Ile His
535      770      775      780
536 Arg Lys Thr Thr Ala Ser Thr Arg Lys Val Ser Leu Ala Pro Gln Ala
537 785      790      795      800
538 Asn Leu Thr Glu Leu Asp Ile Tyr Ser Arg Arg Leu Ser Gln Glu Thr
539      805      810      815
540 Gly Leu Glu Ile Ser Glu Glu Ile Asn Glu Glu Asp Leu Lys Glu Cys
541      820      825      830
542 Leu Phe Asp Asp Met Glu Ser Ile Pro Ala Val Thr Thr Trp Asn Thr

```

RAW SEQUENCE LISTING  
 PATENT APPLICATION: US/09/405,735

DATE: 05/09/2000  
 TIME: 11:10:38

Input Set : A:\Seqlist.txt  
 Output Set: N:\CRF3\05092000\I405735.raw

```

543      835      840      845
544 Tyr Leu Arg Tyr Ile Thr Val His Lys Ser Leu Ile Phe Val Leu Ile
545      850      855      860
546 Trp Cys Leu Val Ile Phe Leu Ala Glu Val Ala Ala Ser Leu Val Val
547 865      870      875      880
548 Leu Trp Leu Leu Gly Asn Thr Pro Leu Gln Asp Lys Gly Asn Ser Thr
549      885      890      895
550 His Ser Arg Asn Asn Ser Tyr Ala Val Ile Ile Thr Ser Thr Ser Ser
551      900      905      910
552 Tyr Tyr Val Phe Tyr Ile Tyr Val Gly Val Ala Asp Thr Leu Leu Ala
553      915      920      925
554 Met Gly Phe Phe Arg Gly Leu Pro Leu Val His Thr Leu Ile Thr Val
555      930      935      940
556 Ser Lys Ile Leu His His Lys Met Leu His Ser Val Leu Gln Ala Pro
557 945      950      955      960
558 Met Ser Thr Leu Asn Thr Leu Lys Ala Gly Gly Ile Leu Asn Arg Phe
559      965      970      975
560 Ser Lys Asp Ile Ala Ile Leu Asp Asp Leu Leu Pro Leu Thr Ile Phe
561      980      985      990
562 Asp Phe Ile Gln Leu Leu Leu Ile Val Ile Gly Ala Ile Ala Val Val
563      995      1000      1005
564 Ala Val Leu Gln Pro Tyr Ile Phe Val Ala Thr Val Pro Val Ile Val
565      1010      1015      1020
566 Ala Phe Ile Met Leu Arg Ala Tyr Phe Leu Gln Thr Ser Gln Gln Leu
E--> 567 1025      1030      1035      1040
568 Lys Gln Leu Glu Ser Glu Gly Arg Ser Pro Ile Phe Thr His Leu Val
569      1045      1050      1055
570 Thr Ser Leu Lys Gly Leu Trp Thr Leu Arg Ala Phe Gly Arg Gln Pro
571      1060      1065      1070
572 Tyr Phe Glu Thr Leu Phe His Lys Ala Leu Asn Leu His Thr Ala Asn
573      1075      1080      1085
574 Trp Phe Leu Tyr Leu Ser Thr Leu Arg Trp Phe Gln Met Arg Ile Glu
575      1090      1095      1100
576 Met Ile Phe Val Ile Phe Phe Ile Ala Val Thr Phe Ile Ser Ile Leu
E--> 577 1105      1110      1115      1120
578 Thr Thr Gly Glu Gly Glu Gly Arg Val Gly Ile Ile Leu Thr Leu Ala
579      1125      1130      1135
580 Met Asn Ile Met Ser Thr Leu Gln Trp Ala Val Asn Ser Ser Ile Asp
581      1140      1145      1150
582 Val Asp Ser Leu Met Arg Ser Val Ser Arg Val Phe Lys Phe Ile Asp
583      1155      1160      1165
584 Met Pro Thr Glu Gly Lys Pro Thr Lys Ser Thr Lys Pro Tyr Lys Asn
585      1170      1175      1180
586 Gly Gln Leu Ser Lys Val Met Ile Ile Glu Asn Ser His Val Lys Lys
E--> 587 1185      1190      1195      1200
588 Asp Asp Ile Trp Pro Ser Gly Gly Gln Met Thr Val Lys Asp Leu Thr
589      1205      1210      1215
590 Ala Lys Tyr Thr Glu Gly Gly Asn Ala Ile Leu Glu Asn Ile Ser Phe
591      1220      1225      1230

```

RAW SEQUENCE LISTING  
 PATENT APPLICATION: US/09/405,735

DATE: 05/09/2000  
 TIME: 11:10:38

Input Set : A:\Seqlist.txt  
 Output Set: N:\CRF3\05092000\I405735.raw

```

592 Ser Ile Ser Pro Gly Gln Arg Val Gly Leu Leu Gly Arg Thr Gly Ser
593      1235      1240      1245
594 Gly Lys Ser Thr Leu Leu Ser Ala Phe Leu Arg Leu Leu Asn Thr Glu
595      1250      1255      1260
596 Gly Glu Ile Gln Ile Asp Gly Val Ser Trp Asp Ser Ile Thr Leu Gln
E--> 597 1265      1270      1275      1280
598 Gln Trp Arg Lys Ala Phe Gly Val Ile Pro Gln Lys Val Phe Ile Phe
599      1285      1290      1295
600 Ser Gly Thr Phe Arg Lys Asn Leu Asp Pro Tyr Glu Gln Trp Ser Asp
601      1300      1305      1310
602 Gln Glu Ile Trp Lys Val Ala Asp Glu Val Gly Leu Arg Ser Val Ile
603      1315      1320      1325
604 Glu Gln Phe Pro Gly Lys Leu Asp Phe Val Leu Val Asp Gly Gly Cys
605      1330      1335      1340
606 Val Leu Ser His Gly His Lys Gln Leu Met Cys Leu Ala Arg Ser Val
E--> 607 1345      1350      1355      1360
608 Leu Ser Lys Ala Lys Ile Leu Leu Leu Asp Glu Pro Ser Ala His Leu
609      1365      1370      1375
610 Asp Pro Val Thr Tyr Gln Ile Ile Arg Arg Thr Leu Lys Gln Ala Phe
611      1380      1385      1390
612 Ala Asp Cys Thr Val Ile Leu Cys Glu His Arg Ile Glu Ala Met Leu
613      1395      1400      1405
614 Glu Cys Gln Gln Phe Leu Val Ile Glu Glu Asn Lys Val Arg Gln Tyr
615      1410      1415      1420
616 Asp Ser Ile Gln Lys Leu Leu Asn Glu Arg Ser Leu Phe Arg Gln Ala
E--> 617 1425      1430      1435      1440
618 Ile Ser Pro Ser Asp Arg Val Lys Leu Phe Pro His Arg Asn Ser Ser
619      1445      1450      1455
620 Lys Cys Lys Ser Lys Pro Gln Ile Ala Ala Leu Lys Glu Glu Thr Glu
621      1460      1465      1470
622 Glu Glu Val Gln Asp Thr Arg Leu
623      1475      1480

```

VERIFICATION SUMMARY  
PATENT APPLICATION: US/09/405,735

DATE: 05/09/2000  
TIME: 11:10:39

Input Set : A:\Seqlist.txt  
Output Set: N:\CRF3\05092000\I405735.raw

L:303 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:323 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:343 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:363 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:383 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:403 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:430 M:254 E: (42) Number of Bases conflicts Running Total, LENGTH:Input:1 Counted:6129  
L:567 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:2  
M:332 Repeated in SeqNo=2